



## **RAW SEQUENCE LISTING ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/798,096A  
Source: IFWO  
Date Processed by STIC: 7/27/04

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

**Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:**

- 1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202**

Revised 05/17/04

# Raw Sequence Listing Error Summary

| ERROR DETECTED   | SUGGESTED CORRECTION   | SERIAL NUMBER: 10/798,096A |
|--|--|----------------------------|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE |  |                            |
| 1 <input checked="" type="checkbox"/> Wrapped Nucleics<br>Wrapped Aminos                             | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."   |                            |
| 2 <input type="checkbox"/> Invalid Line Length   | The rules require that a line not exceed 72 characters in length. This includes white spaces.  |                            |
| 3 <input type="checkbox"/> Misaligned Amino Numbering  | The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  |                            |
| 4 <input type="checkbox"/> Non-ASCII   | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.   |                            |
| 5 <input type="checkbox"/> Variable Length   | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.   |                            |
| 6 <input type="checkbox"/> PatentIn 2.0<br>"bug"   | A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.  |                            |
| 7 <input type="checkbox"/> Skipped Sequences<br>(OLD RULES)  | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO: X: (insert SEQ ID NO where "X" is shown)<br>(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading.)<br>(ii) SEQUENCE DESCRIPTION: SEQ ID NO: X: (insert SEQ ID NO where "X" is shown)<br>This sequence is intentionally skipped<br><br>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |                            |
| 8 <input type="checkbox"/> Skipped Sequences<br>(NEW RULES)  | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:<br><210> sequence id number<br><400> sequence id number<br>000   |                            |
| 9 <input type="checkbox"/> Use of n's or Xaa's<br>(NEW RULES)  | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents  |                            |
| 10 <input type="checkbox"/> Invalid <213><br>Response  | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence   |                            |
| 11 <input type="checkbox"/> Use of <220>   | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 0001/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)  |                            |
| 12 <input type="checkbox"/> PatentIn 2.0<br>"bug"  | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.  |                            |
| 13 <input type="checkbox"/> Misuse of n/Xaa  | "n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>  |                            |



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/798,096A

DATE: 07/27/2004

TIME: 11:56:44

Input Set : A:\pto.lm.TXT

Output Set: N:\CRF4\07272004\J798096A.raw

3 <110> APPLICANT: Rea-Min Chu  
 4 Ching-Yi Lin  
 5 Ya-Wen Hsiao  
 6 Kuang-Wen Liao  
 W--> 7 <120> TITLE OF INVENTION: COMPLEX IMMUNO-GENE MEDICAL COMPOSITION FOR INHIBITING TUMOR CELLS  
 W--> 8 <130> FILE REFERENCE: P/741-176  
 W--> 9 <140> CURRENT APPLICATION NUMBER: 10/798,096A  
 10 <141> CURRENT FILING DATE: 2004-03-11  
 W--> 11 <160> NUMBER OF SEQ ID: 4

## ERRORED SEQUENCES

*mandatory, please insert (220), whenever (221), (222) on (223) is present.*

*PLEASE see item # 1 on error summary sheet.*

*Does Not Comply Corrected Diskette Needed (pg. 1-3)*

*only 16 codons are valid per line*

13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 636  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Human  
 17 <223> OTHER INFORMATION: IL-6  
 E--> 19 <400> SEQUENCE: 1  
 21 atg aac tcc ttc tcc aca agc gcc ttc ggt cca gtt gcc tcc tcc ctg ggg ctg ctc ctg  
 22 60  
 23 Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu Gly Leu Leu Leu  
 24 1 5 10 15 20  
 E--> 26 gtg ctg cct gct gcc ttc cct gcc cca gta ccc cca gga gaa gat tcc aaa gat gta gcc  
 27 120  
 28 Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala  
 29 25 30 35 40  
 E--> 31 gcc cca cac aga cag cca ctc acc tct tca gaa cga att gac aaa caa att cgg tac atc  
 32 180  
 33 Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile  
 34 45 50 55 60  
 E--> 36 ctg gac ggc atc tca gcc ctg aga aag gag aca tgt aac aag agt aac atg tgt gaa  
 37 agc 240  
 38 Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser  
 39 65 70 75 80  
 E--> 41 agc aaa gag gca ctg gca gaa aac aac ctg aac ctt cca aag atg gct gaa aaa gat gga  
 42 300  
 43 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp  
 W--> 44 Gly  
 W--> 45 85 90 95 100  
 E--> 47 tgc ttc caa tct gga ttc aat gag gag act tgc ctg gtg aaa atc atc act ggt ctt ttg  
 48 360  
 49 Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu

## RAW SEQUENCE LISTING

DATE: 07/27/2004

PATENT APPLICATION: US/10/798,096A

TIME: 11:56:44

Input Set : A:\pto.lm.TXT

Output Set: N:\CRF4\07272004\J798096A.raw

W--> 50 105 110 115 120  
E--> 52 gag ttt gag gta tac cta cag tac ctc cag aac aga ttt gag agt agt gag gaa caa gcc  
53 420  
54 Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala  
W--> 55 125 130 135 140  
E--> 57 aga gct gtg cag atg agt aca aaa gtc ctg atc cag ttc ctg cag aaa aag gca aag aat  
58 480  
59 Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn  
W--> 60 145 150 155 160  
E--> 62 cta gat gca ata acc acc cct gac cca acc aca aat gcc agc ctg ctg acg aag ctg cag  
63 540  
64 Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln  
W--> 65 165 170 175 180  
E--> 67 gca cag aac cag tgg ctg cag gac atg aca act cat ctc att ctg cgc agc ttt aag gag  
68 600  
69 Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu  
W--> 70 185 190 195 200  
E--> 72 ttc gtg cag tcc agc ctg agg gct ctt cgg caa atg  
73 636  
74 Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met  
W--> 75 205 210  
77 <210> SEQ ID NO: 2  
78 <211> LENGTH: 60  
79 <212> TYPE: DNA  
80 <213> ORGANISM: Human  
81 <223> OTHER INFORMATION: IL-2 Signal Peptide  
E--> 83 <400> SEQUENCE: 2  
E--> 85 atg tac agg atg caa ctc ctg tct tgc att gca cta agt ctt gca ctt gtc aca aac agt  
86 60  
87 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser  
88 1 5 10 15 20  
91 <210> SEQ ID NO: 3  
92 <211> LENGTH: 342  
93 <212> TYPE: DNA  
94 <213> ORGANISM: Human  
95 <223> OTHER INFORMATION: Partial Sequence Encoding Human IL-15  
97 <400> SEQUENCE: 3  
E--> 99 aac tgg gtg aat gta ata agt gat ttg aaa aaa att gaa gat ctt att caa tct atg cat  
100 60  
101 Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His  
102 1 5 10 15 20  
E--> 104 att gat gct act tta tat acg gaa agt gat gtt cac ccc agt tgc aaa gta aca gca atg  
105 120  
106 Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met  
107 25 30 35 40  
E--> 109 aag tgc ttt ctc ttg gag tta caa gtt att tca ctt gag tcc gga gat gca agt att cat  
110 180  
111 Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His  
112 45 50 55 60

please insert  
<220> whenever <221>, <222> or <223>  
is present.

insert  
<220> same error

only  
16  
codons  
valid  
per  
line.

cl  
fem  
on  
error  
in  
sheet

## RAW SEQUENCE LISTING

DATE: 07/27/2004

PATENT APPLICATION: US/10/798,096A

TIME: 11:56:44

Input Set : A:\pto.lm.TXT

Output Set: N:\CRF4\07272004\J798096A.raw

```

E--> 114 gat aca gta gaa aat ctg atc atc cta gca aac aac agt ttg tct tct aat ggg aat gta
      115 240
      116 Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
W--> 117 Val
W--> 118          65          70          75          80
E--> 120 aca gaa tct gga tgc aaa gaa tgt gag gaa ctg gag gaa aaa aat att aaa gaa ttt ttg
      121 300
      122 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
W--> 123          85          90          95          100
E--> 125 gag agt ttt gta cat att gtc caa atg ttc atc aac act tct
      126 342
      127 Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
W--> 128          105          110
      131 <210> SEQ ID NO: 4
      132 <211> LENGTH: 402
      133 <212> TYPE: DNA
      134 <213> ORGANISM: Artificial Sequence
W--> 135 <220> FEATURE: Bases 1-60 Code for IL-2 Signal Peptide
W--> 136 <220> FEATURE: Bases 1-60 Code for IL-2 Signal Peptide
      136 <223> OTHER INFORMATION: Artificial Chimeric Sequence Encoding IL-2SP/IL-15MP
      138 <400> SEQUENCE: 4
E--> 140 agt tac agg atg caa ctc ctg tct tgc att gca cta agt ctt gca ctt gtc aca aac agt
      141 60
      142 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
      143 1          5          10          15          20
E--> 145 aga tgg gtg aat gta ata agt gat ttg aaa aaa att gaa gat ctt att caa tct atg cat
      146 120
      147 Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
      148          25          30          35          40
E--> 150 att gat gct act tta tat acg gaa agt gat gtt cac ccc agt tgc aaa gta aca gca atg
      151 180
      152 Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
      153          45          50          55          60
E--> 155 aag tgc ttt ctc ttg gag tta caa gtt att tca ctt gag tcc gga gat gca agt att cat
      156 240
      157 Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
      158          65          70          75          80
E--> 160 gat aca gta gaa aat ctg atc atc cta gca aac aac agt ttg tct tct aat ggg aat gta
      161 300
      162 Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
      163          85          90          95          100
E--> 165 aca gaa tct gga tgc aaa gaa tgt gag gaa ctg gag gaa aaa aat att aaa gaa ttt ttg
      166 360
      167 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
      168          105          110          115          120
E--> 170 gag agt ttt gta cat att gtc caa atg ttc atc aac act tct
      171 402
      172 Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
      173          125          130

```

delete  
 Same error  
 Please do not insert  
 a response before  
 numeric  
 identifier  
 2202

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 07/27/2004  
PATENT APPLICATION: US/10/798,096A      TIME: 11:56:45

Input Set : A:\pto.lm.TXT  
Output Set: N:\CRF4\07272004\J798096A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 21,23,26,28,31,33,38,64,72  
Seq#:2; Line(s) 87  
Seq#:3; Line(s) 101,106,111,122,125  
Seq#:4; Line(s) 142,147,152,157,162,167

## VERIFICATION SUMMARY

DATE: 07/27/2004

PATENT APPLICATION: US/10/798,096A

TIME: 11:56:45

Input Set : A:\pto.lm.TXT

Output Set: N:\CRF4\07272004\J798096A.raw

L:7 M:283 W: Missing Blank Line separator, <120> field identifier  
L:8 M:283 W: Missing Blank Line separator, <130> field identifier  
L:9 M:283 W: Missing Blank Line separator, <140> field identifier  
L:11 M:283 W: Missing Blank Line separator, <160> field identifier  
L:19 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1  
L:21 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1  
L:26 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:1  
L:31 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:180 SEQ:1  
L:36 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:237 SEQ:1  
L:41 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:1  
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:47 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:360 SEQ:1  
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:52 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:420 SEQ:1  
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:57 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:480 SEQ:1  
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:62 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:540 SEQ:1  
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:67 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:600 SEQ:1  
L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:72 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:636 SEQ:1  
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:83 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:2  
L:85 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:2  
L:97 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3  
L:99 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3  
L:104 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:3  
L:109 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:180 SEQ:3  
L:114 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:240 SEQ:3  
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:120 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:3  
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:125 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:342 SEQ:3  
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:135 M:283 W: Missing Blank Line separator, <220> field identifier  
L:135 M:256 W: Invalid Numeric/Header Field, <220> has non-blank data  
L:140 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:4  
L:145 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:4  
L:150 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:180 SEQ:4  
L:155 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:240 SEQ:4  
L:160 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:4  
L:165 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:360 SEQ:4  
L:170 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:402 SEQ:4